

HPV58

A transcription map of HPV58 early genes deduced from HPV58-infected cervical tissues (1). A linear version of the updated HPV58 genome is shown at the top of the figure. Indicated are early (AE) and late (AL) poly (A) signals. LCR indicates the Long Control Region or URR (Upstream Regulatory Region). A putative TATA box-containing promoter (P) at nt 72 is represented by a bent arrow. Boxes in the top half of the figure represent the indicated ORFs, with the first nucleotide position of the initiation codon and the last nucleotide position of the stop codon given. The nucleotide positions in the E4 and L1 ORFs in the newly assigned reading frames 3 and 2 have been updated from a previous publication (2). Due to these changes, we have also reassigned the E6, E2, and L2 ORFs into reading frame 1 and the E7, E1, and E5 ORFs into reading frame 3. Below the central box (lines A to E) are the RNA species deduced from alternative RNA splicing of viral early transcripts based on the results of RNA splicing assays. Coding potentials for each RNA species are shown on the right.

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1. Li, Y., Wang, X., Ni, T., Wang, F., Lu, W., Zhu, J., Xie, X and Zheng, Z-M.

Human Papillomavirus Type 58 Genome Variations and RNA Expression in Cervical Lesions

2. Kirii Y, Iwamoto S, Matsukura T. Human papillomavirus type 58 DNA sequence. *Virology* **185**:424–427 (1991)

J. Virol. **87**: 9313–9322 (2012)